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Erratum

Phylogenomics Resolves Evolutionary Relationships among Ants, Bees, and Wasps

Brian R. Johnson, Marek L. Borowiec, Joanna C. Chiu, Ernest K. Lee, Joel Atallah, and Philip S. Ward*

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In our recent paper on the phylogeny of aculeate Hymenoptera, we supplemented our primary data set with publicly available genome sequence data from four bee species, three ant species, and one wasp species. However, we did not give detailed citations for these data, nor did we make a clear distinction between those species whose genomes had been formally published and those for which data had been made publicly available prior to publication. The published genomes were those of the wasp *Nasonia vitripennis* [1], the honeybee *Apis mellifera* [2], and the ants *Harpegnathos saltator* [3], *Pogonomyrmex barbatus* [4], and *Linepithema humile* [5]. The prepublication genome data came from the bees *Lasioglossum albipes* (NCBI Sequence Read Archive SRR578269, as part of the *Lasioglossum albipes* WGS project, http://www.ncbi.nlm.nih.gov/bioproject/174755), *Megachile rotundata* (NCBI Protein database search, with data coming mostly from the *Megachile* genome sequencing project, http://www.ncbi.nlm.nih.gov/bioproject/66515), and *Bombus terrestris* (protein set from NCBI RefSeq and Genome Annotation projects, derived from genomic sequence generated by the Bumble Bee Genome Project, https://www.hgsc.bcm.edu/arthropods/bumble-bee-genome-project).

We apologize for any confusion created by the lack of explicit citations of these data sources.

References

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*Correspondence: psward@ucdavis.edu

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